

Figure 1A

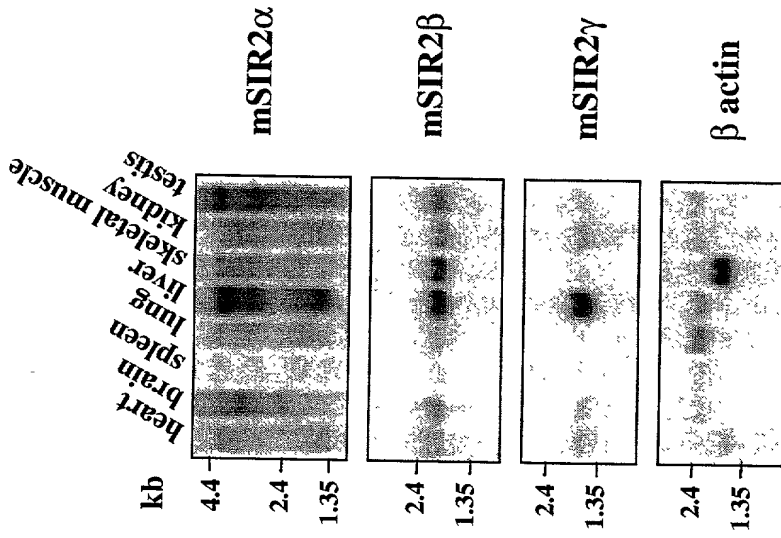


Figure 1B

|        |     |              |     |                |             |     |
|--------|-----|--------------|-----|----------------|-------------|-----|
| ySIR2  | 1   | TNKKVIGT     | 30  | IRLSNEFTIDHE   | QKHTIA      | 61  |
| yHST1  | 1   | TNKKVIGT     | 30  | IRLSNEFTIDHE   | QKHTIA      | 61  |
| mSIR2α | 1   | MINILSEPPK   | 33  | IRLSNEFTIDHE   | QKHTIA      | 61  |
| Cobb   | 1   | MINILSEPPK   | 33  | IRLSNEFTIDHE   | QKHTIA      | 61  |
|        |     | *****        |     | *****          |             |     |
| ySIR2  | 31  | LVLTGAGVSTSL | 61  | GIPDFRSSEGEFYS | ---         | 93  |
| yHST1  | 31  | LVLTGAGVSTSL | 61  | GIPDFRSSEGEFYS | ---         | 93  |
| mSIR2α | 34  | LVLTGAGVSTSL | 61  | GIPDFRSSEGEFYS | ---         | 93  |
| Cobb   | 8   | LVLTGAGVSTSL | 61  | GIPDFRSSEGEFYS | ---         | 93  |
|        |     | *****        |     | *****          |             |     |
| ySIR2  | 62  | LDPDQDVIRAN  | 93  | YFNIMHDPFYS    | YFNIMHDPFYS | 93  |
| yHST1  | 62  | LDPDQDVIRAN  | 93  | YFNIMHDPFYS    | YFNIMHDPFYS | 93  |
| mSIR2α | 67  | LDPDQDVIRAN  | 93  | YFNIMHDPFYS    | YFNIMHDPFYS | 93  |
| Cobb   | 39  | VATIEGEFARN  | 68  | PGLVQT---      | FYNARRQQLQ  | 68  |
|        |     | *****        |     | *****          |             |     |
| ySIR2  | 94  | YSPLHRSIF    | 125 | KMLQMK         | KGKLLRN     | 125 |
| yHST1  | 94  | YSPLHRSIF    | 125 | KMLQMK         | KGKLLRN     | 125 |
| mSIR2α | 99  | YSPLHRSIF    | 125 | KMLQMK         | KGKLLRN     | 125 |
| Cobb   | 69  | YSPLHRSIF    | 125 | KMLQMK         | KGKLLRN     | 125 |
|        |     | *****        |     | *****          |             |     |
| ySIR2  | 126 | AGTSTDKLV    | 158 | QCHGSFATAS     | CVTCHWNLP   | 158 |
| yHST1  | 126 | AGTSTDKLV    | 158 | QCHGSFATAS     | CVTCHWNLP   | 158 |
| mSIR2α | 131 | AGTSTDKLV    | 158 | QCHGSFATAS     | CVTCHWNLP   | 158 |
| Cobb   | 102 | AGTSTDKLV    | 158 | QCHGSFATAS     | CVTCHWNLP   | 158 |
|        |     | *****        |     | *****          |             |     |
| ySIR2  | 159 | NKTRNLEL     | 188 | YCYKRRREY      | EGYNNKV     | 191 |
| yHST1  | 159 | NKTRNLEL     | 188 | YCYKRRREY      | EGYNNKV     | 191 |
| mSIR2α | 162 | NKTRNLEL     | 188 | YCYKRRREY      | EGYNNKV     | 191 |
| Cobb   | 133 | MPEDKCHCQ    | 158 | CHCQFAP        | LRPHVVM     | 158 |
|        |     | *****        |     | *****          |             |     |
| ySIR2  | 192 | ASOGSMSE     | 224 | RRRYL          | NSYGV       | 224 |
| yHST1  | 192 | ASOGSMSE     | 224 | RRRYL          | NSYGV       | 224 |
| mSIR2α | 197 | ASOGSMSE     | 224 | RRRYL          | NSYGV       | 224 |
| Cobb   | 159 | ASOGSMSE     | 224 | RRRYL          | NSYGV       | 224 |
|        |     | *****        |     | *****          |             |     |
| ySIR2  | 225 | K---         | 252 | IFHKSTIR       | LECDLL      | 252 |
| yHST1  | 225 | K---         | 252 | IFHKSTIR       | LECDLL      | 252 |
| mSIR2α | 198 | K---         | 252 | IFHKSTIR       | LECDLL      | 252 |
| Cobb   | 187 | AGFVH        | 219 | EAKLHGA        | HTVLE       | 219 |
|        |     | *****        |     | *****          |             |     |
| ySIR2  | 253 | SEIVNMV      | 282 | PSHVP          | QVILN       | 282 |
| yHST1  | 253 | SEIVNMV      | 282 | PSHVP          | QVILN       | 282 |
| mSIR2α | 226 | SEIVNMV      | 282 | PSHVP          | QVILN       | 282 |
| Cobb   | 220 | SEIVNMV      | 282 | PSHVP          | QVILN       | 282 |

Figure 2C

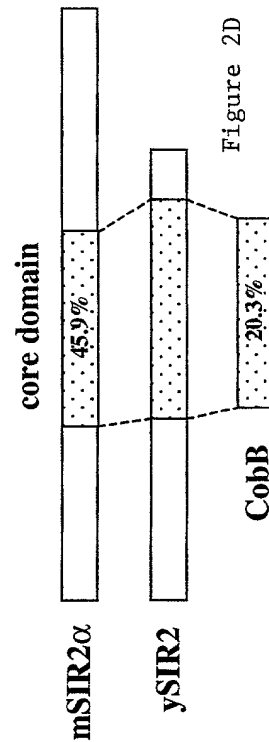


Figure 2B

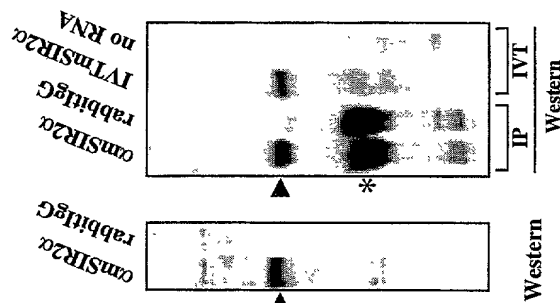


Figure 2A

1 MADEVA LA LQAAGSPSAAAAAMEAASQPADEPLRKRRPRRD;  
41 PGLGRSPGESAAPAAAGCEAASAAAPAA LWREAAGAA  
81 ASAREAPATAVAGDNGSGLRREPRRAADDDEGE  
121 DEAAAAAAAGYRDNLDTGLLTNGFHSCESDDDORT  
161 SHASSDWTPRPRIIGPYTFVQQLMIGTDPRTILKDLLPE  
201 TIPPPELDDMTLWQIVINILSEPPKRRKRDINTIEDAVK  
241 LLOECKIIVLTGAGVSVSCGIPDFRSRGGIYARLAVDFP  
281 DLPDQAMFDIEYRKDRPFFKFAKEIYPGQFQPSLCHK  
321 FIALSDKEGKLLRNYTQNDITLEQVAGIQRI LQCHGSFAT  
361 ASCLICKYKVDCEAVRGDIFNQVVPKRCPCADEPLAI MK  
401 PEIVFFGENLPEQHRAMKYDKDEVLLIVIGSS LKVRPV  
441 ALIPSSIPHEVPQILINREPLPHLHFDVVELLGDGCVIINE  
481 LCHRLGGEYAKLCCNPVKLSEITEKPPRPQKELVHLSLP  
521 PTPPLHISEDSSSPERTVPQDSSVIATLVDAQTNVNDLE  
561 VSESSCVEEKQEVQTSRNVENINVENPDFAVGSSTADK  
601 NERTSVAETVRKWPNR LAKEQISKRLGNQYLFVPPNRY  
641 IFHGAEVSDSEDDVLSSSCGSNSDSGTCSGPSLEEPLE  
681 DESEIEEFYNGLEDTERPEACAGSGFGADGGDQEVVNEA  
721 IATRQELTDVNYPSDKS

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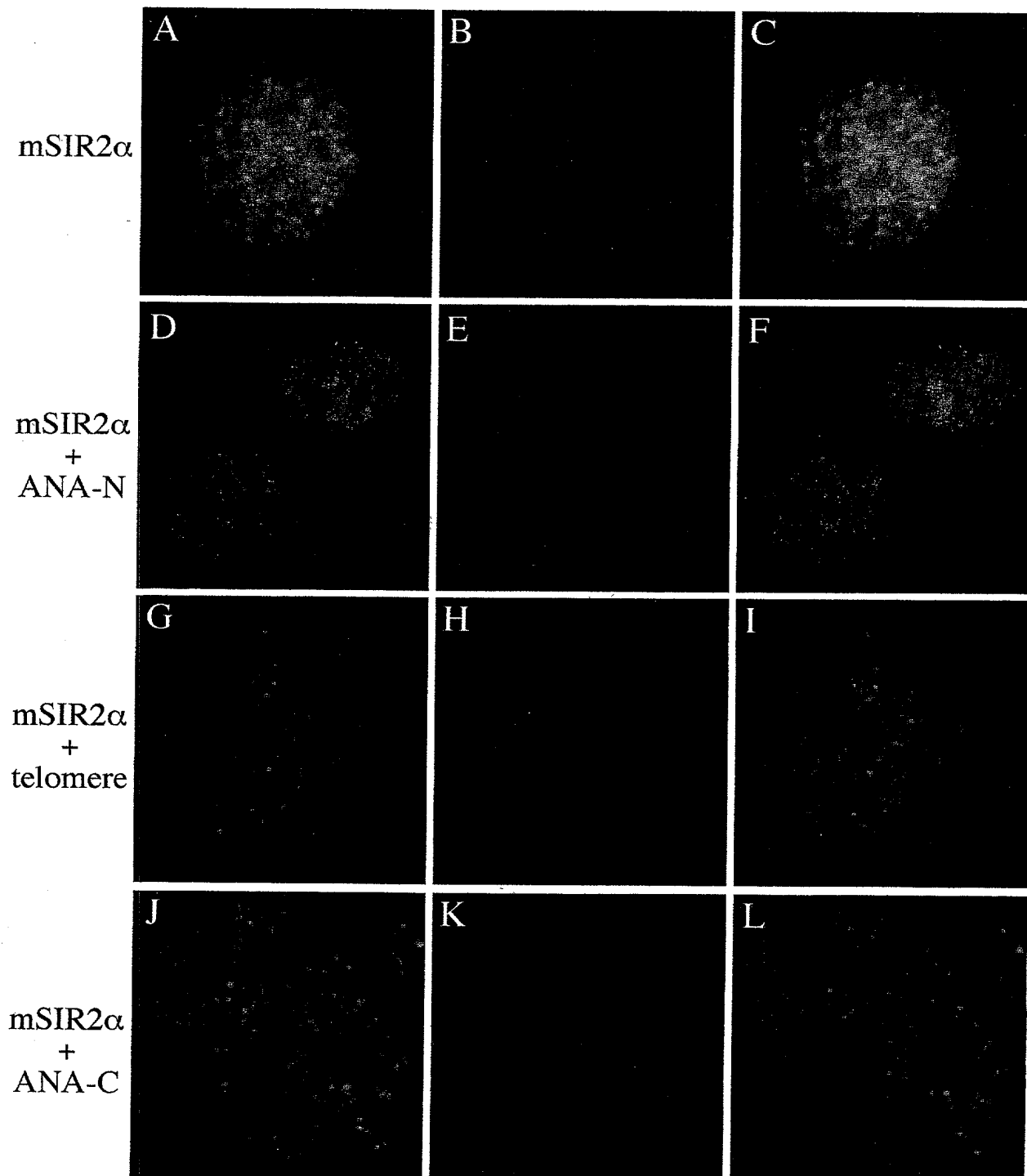


Figure 3

2010-04-09 09:55:50

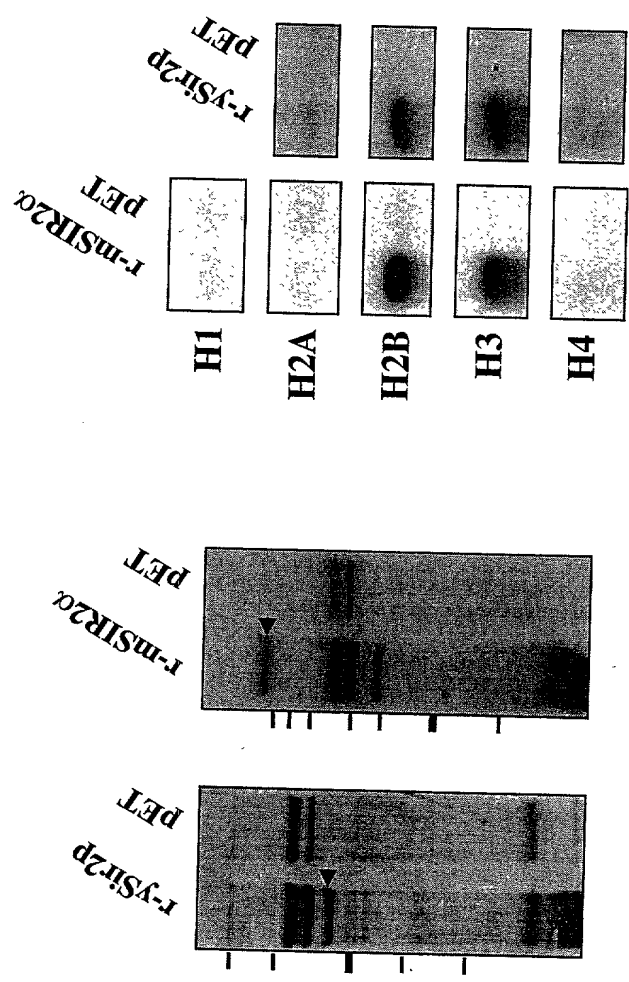


Figure 4A

Figure 4B

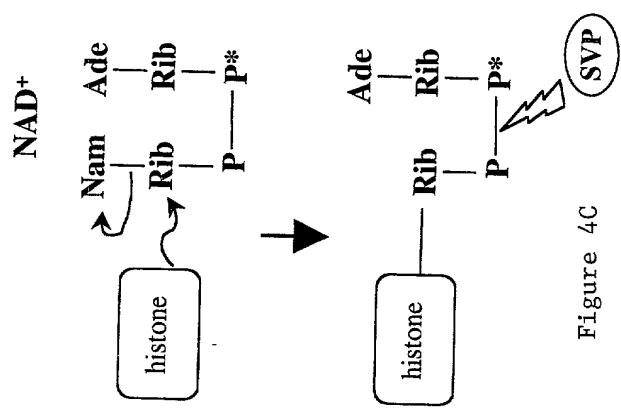


Figure 4C

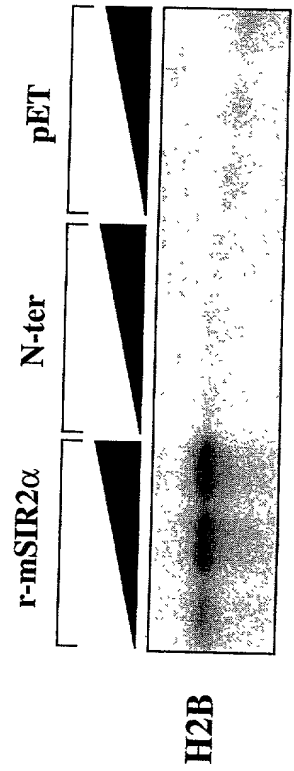


Figure 4D

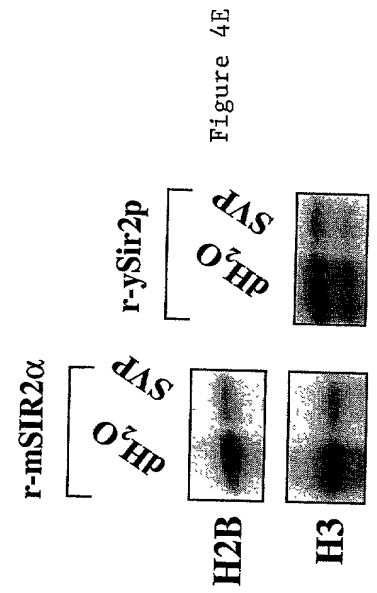


Figure 4E

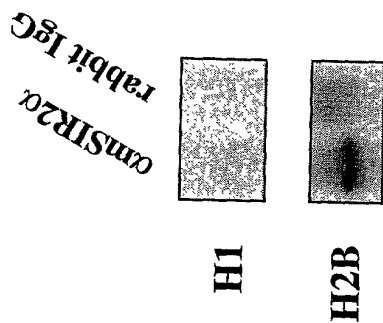


Figure 4G

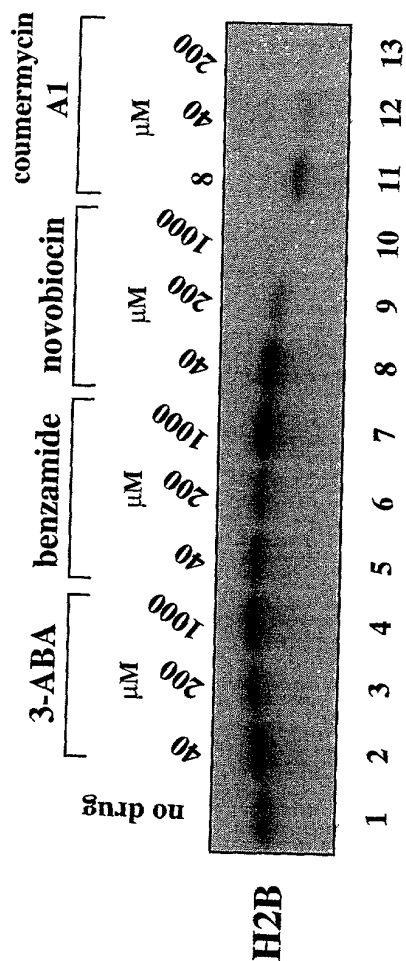


Figure 4F

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unAc                      \*                      \*  
diAc                      ARTKQTARKSTGGKAPRKQLC

|         |                            |          |           |           |          |
|---------|----------------------------|----------|-----------|-----------|----------|
| monoAc  | <b>SGRGKGKGLGKGAKRHRC</b>  | <b>*</b> | <b>*</b>  | <b>*</b>  | <b>*</b> |
|         | <b>5</b>                   | <b>8</b> | <b>12</b> | <b>16</b> |          |
| tetraAc | <b>AGGKGKGKMGKVGAKRHSC</b> | <b>*</b> | <b>*</b>  | <b>*</b>  | <b>*</b> |

PET  
 mSIR2α  
 PET  
 mSIR2α  
 ySIR2p

Figure 5B

2010040" 98/55760

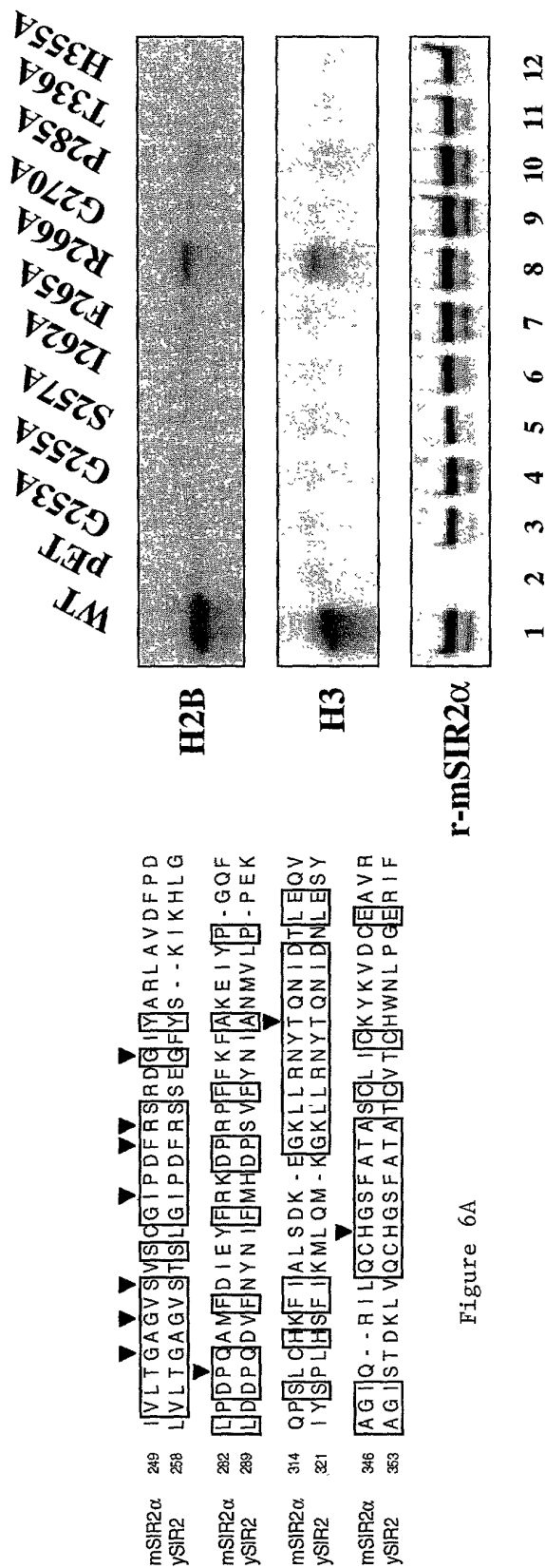


Figure 6A

Figure 6B

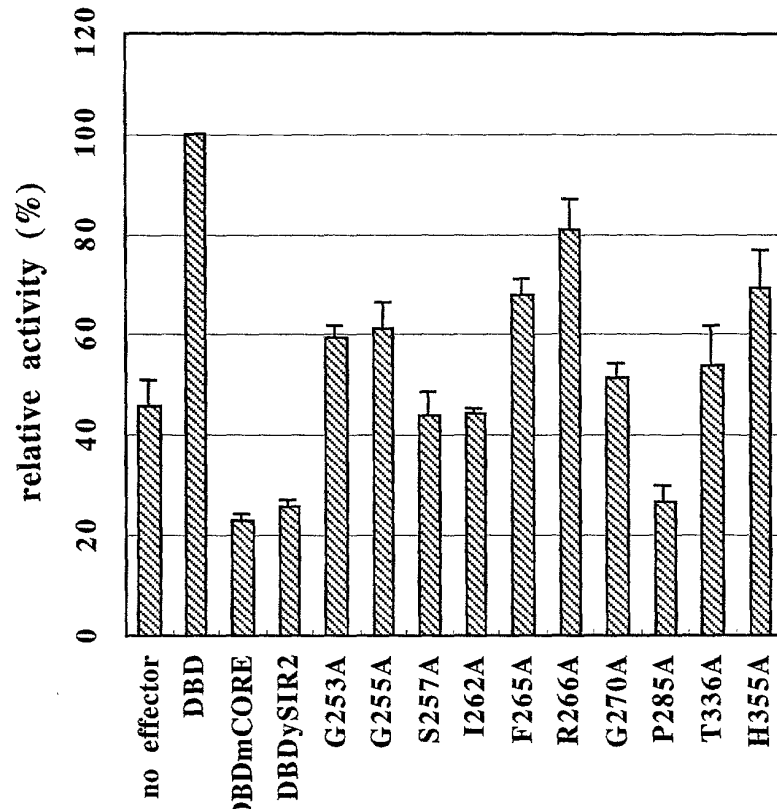


Figure 6D

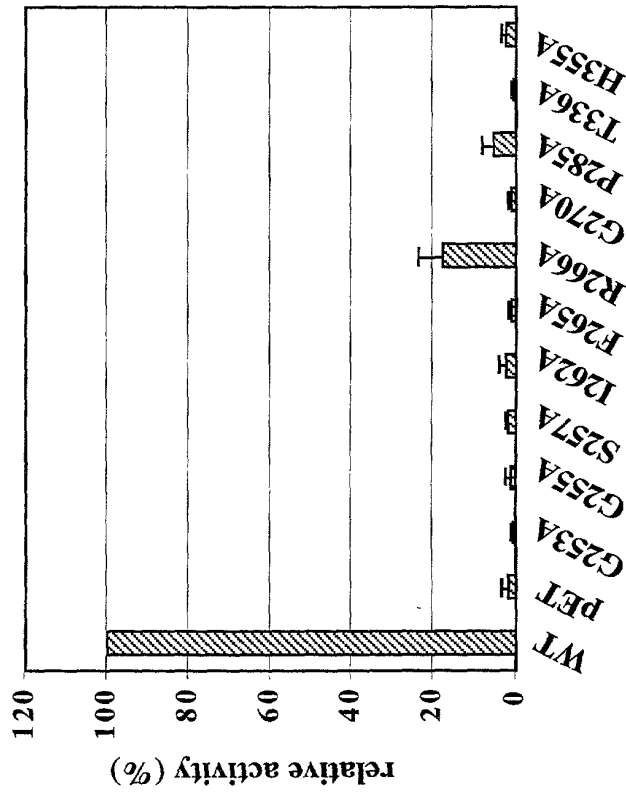


Figure 6C



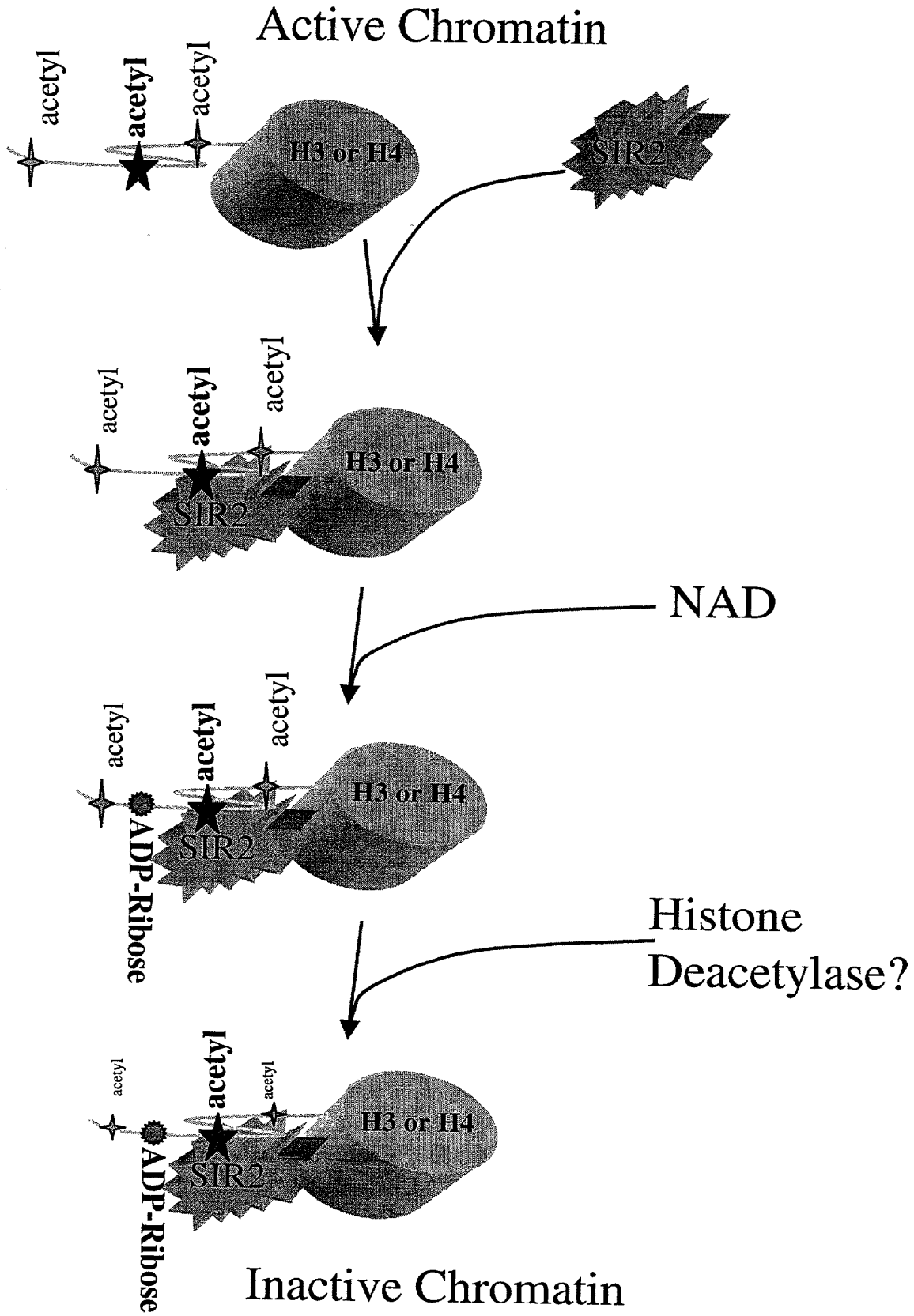


Figure 7

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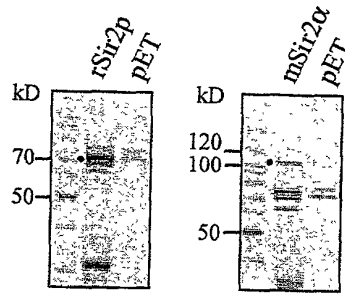


Figure 8a

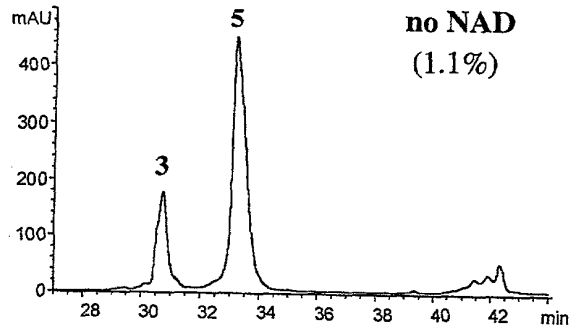


Figure 8b

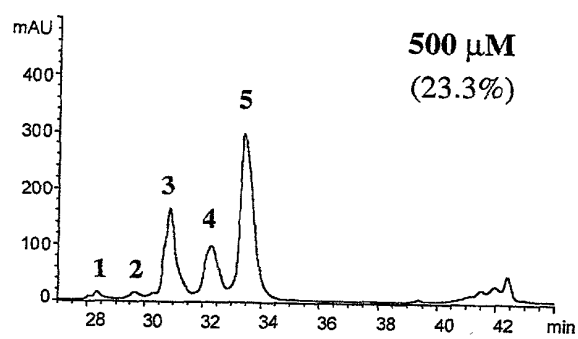


Figure 8e

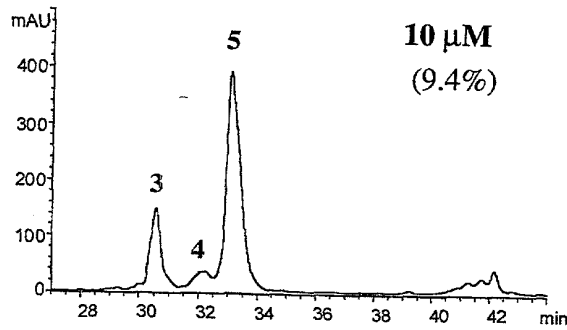


Figure 8c

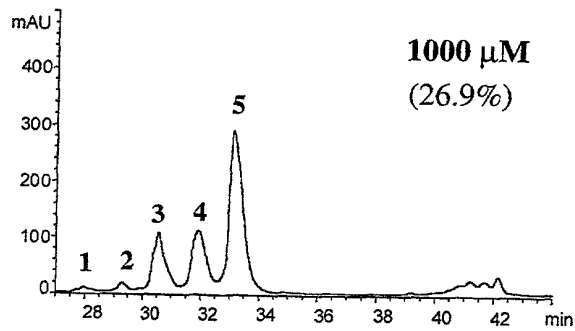


Figure 8f

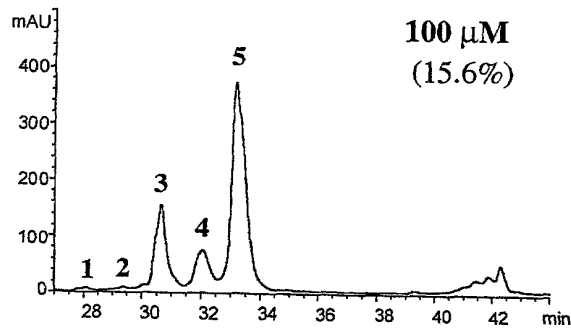


Figure 8d

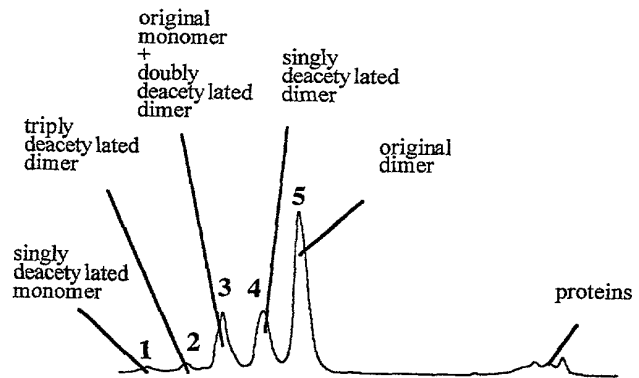


Figure 8g

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Figure 9a

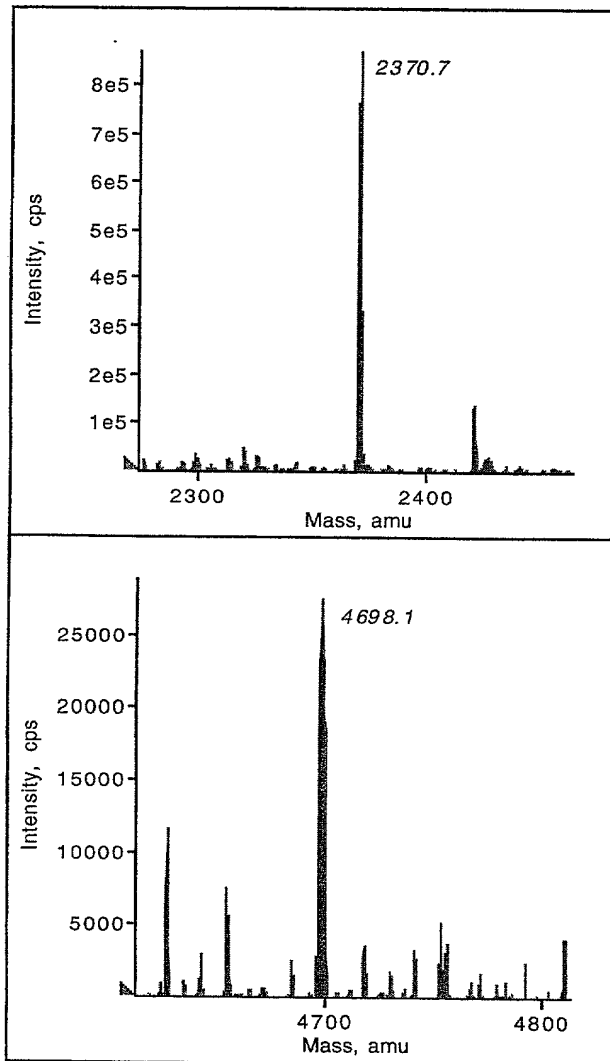


Figure 9b

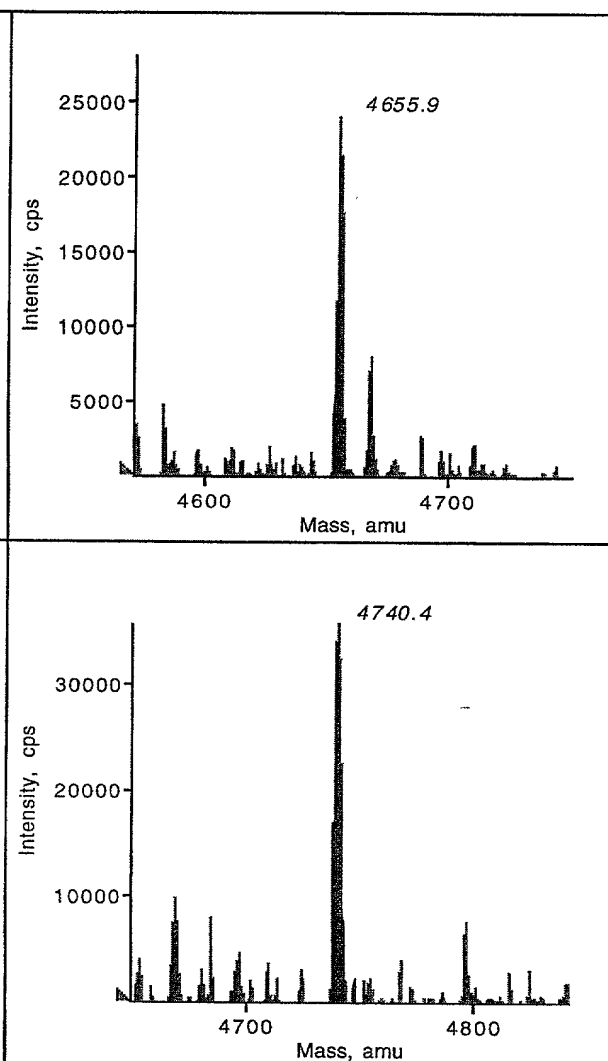


Figure 9c

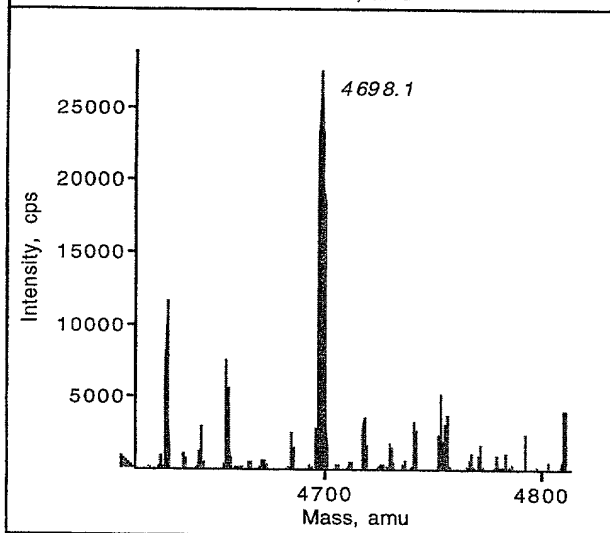
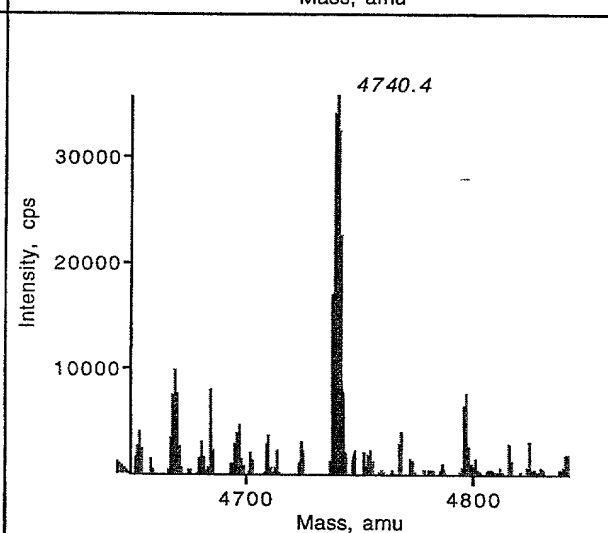


Figure 9d



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201040-9825E/60

peak 4

peak 5

9

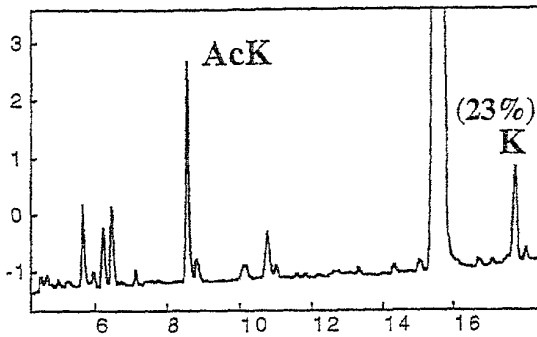


Figure 10a

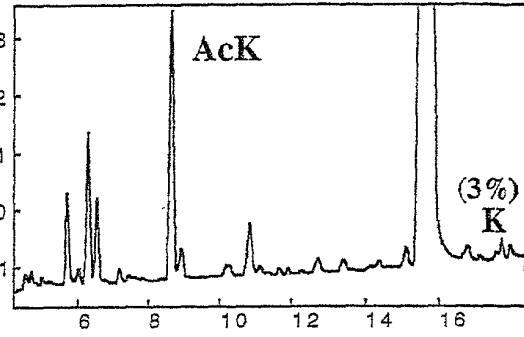


Figure 10d

14

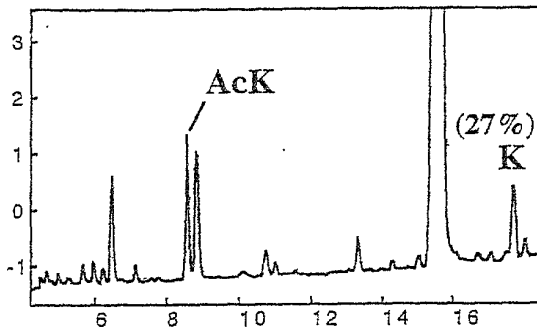


Figure 10b

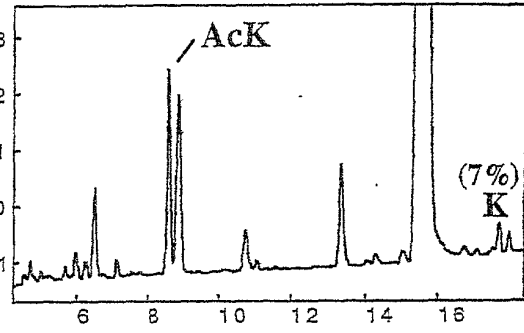


Figure 10e

18

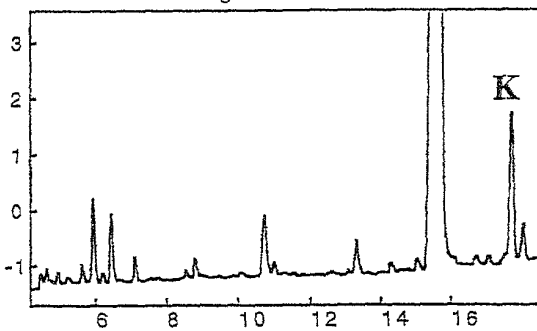


Figure 10c

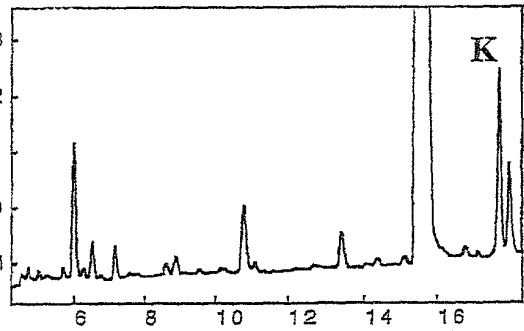


Figure 10f

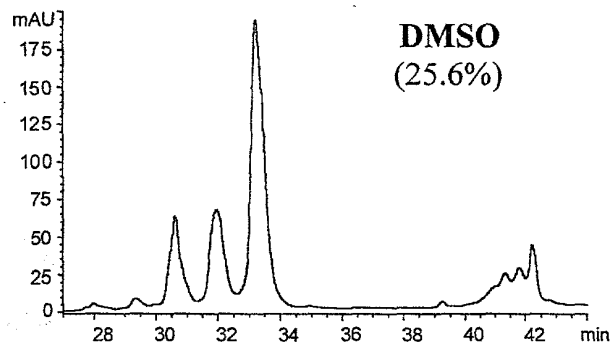


Figure 11a

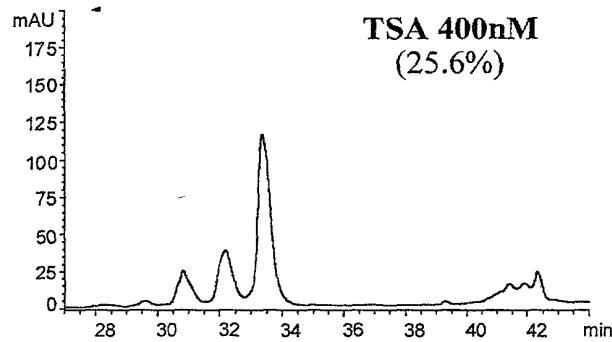


Figure 11b

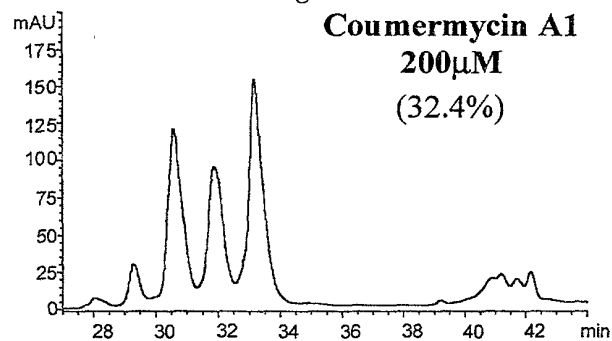


Figure 11e

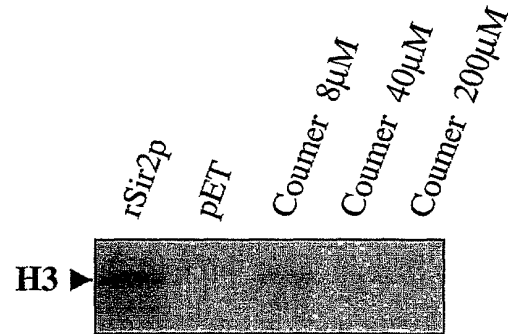


Figure 11c

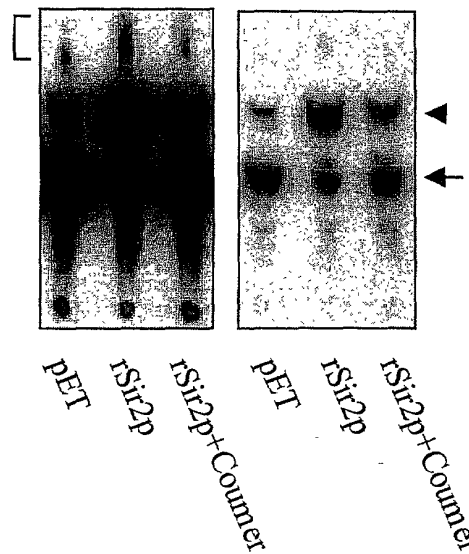


Figure 11d

09/735,786 040402

2010-09-28 22:56:26

1 MADEVALAQAAGSPSAAAAAMEAASQPADEPLRKRPRRDG  
 41 PGLGRSPGEPAAVAPAAAGCEAASAAAPAAALWREAAGAA  
 81 ASAREAPATAVAGDNGSLRREPRAAADDDEDEGE  
 121 DEAAAAAAAI GYRDNL LLDGLLTNGFHSCESDDDRT  
 161 SHASSDWTTPRI GPYTFVQQHLMIGTDPRTI LKDLLPE  
 201 TIPPPELDDMTLWQIVINI LSEPPKRRKRDINTIEDAVK  
 241 LLQECKIIVLTGAGVSVSCGIPDFRSRDGIYARLAVDFP  
 281 DLPDQAMFDIEYFRKDPFPFKFAKEIYPGQFQPSLCHK  
 321 FIALSDKEGKLLRNYTQNI DTLEQVAGIQRI LQCHGSFAT  
 361 ASCLICKYKVDCEAVRGDIFNQVVRGPRCPADEPLAIMK  
 401 PEIVFFGENLPEQFHRAMKYDKDEVLLIVIGSSLKVRPV  
 441 ALIPSSIPHEVPQILINREP LPHLHFDVE LLGDCDVIIINE  
 481 LCHRLGGEYAKLCCNPVKLSEITEKPPRPQKELVH LSELP  
 521 PTPLHISEDSSSPERTVPQDSSV IATLVDQATNNVNDLE  
 561 VSESSCVEEKPOEVQTSRNVENINVENPDFKAVGSGTADK  
 601 NERTSVAETVRKCPNRLAKEQISKRLEGNQYLFVPPNRY  
 641 IFHGAEVYSDSEDDVLSSSSCGNSDSGT CQSPSLEEPLE  
 681 DESEIEEFYNGLEDDETERPECAGSGFGADGGDDQEVVNEA  
 721 IATRQELTDVNYPSDKS

Figure 12a

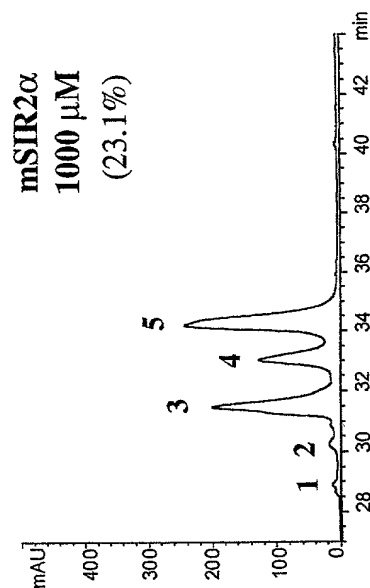


Figure 12c

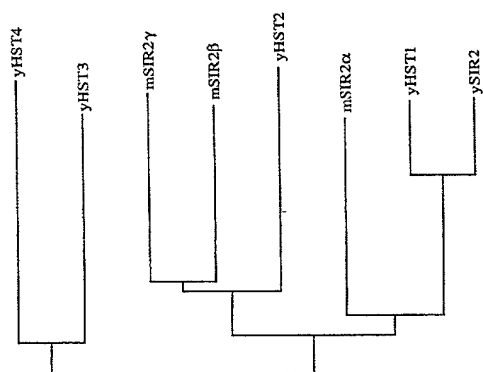


Figure 12b

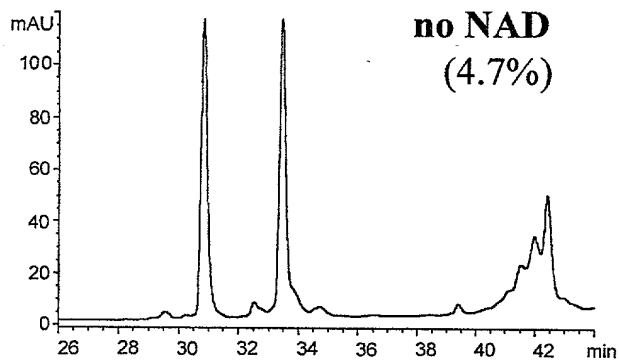


Figure 13a

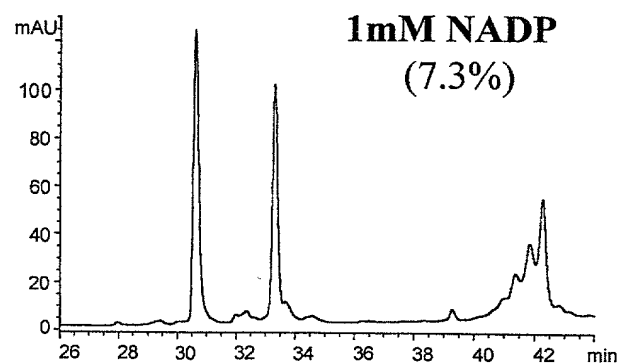


Figure 13d

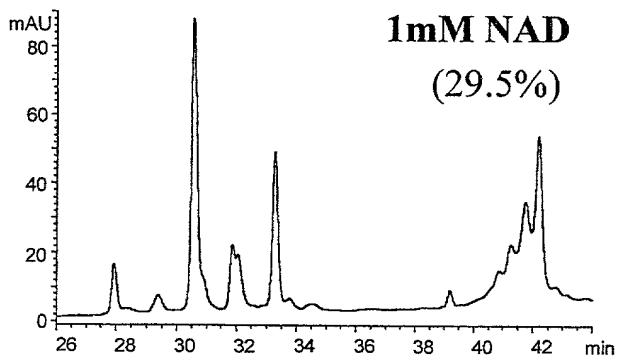


Figure 13b

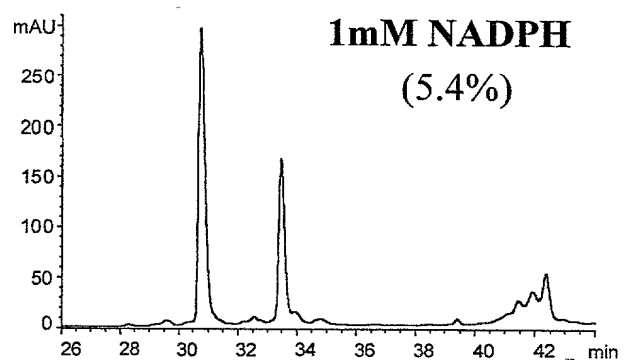


Figure 13e

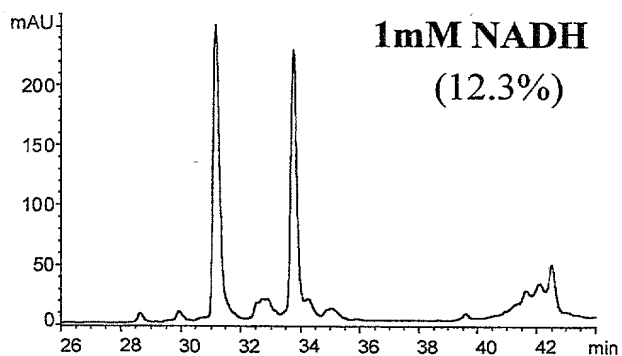


Figure 13c

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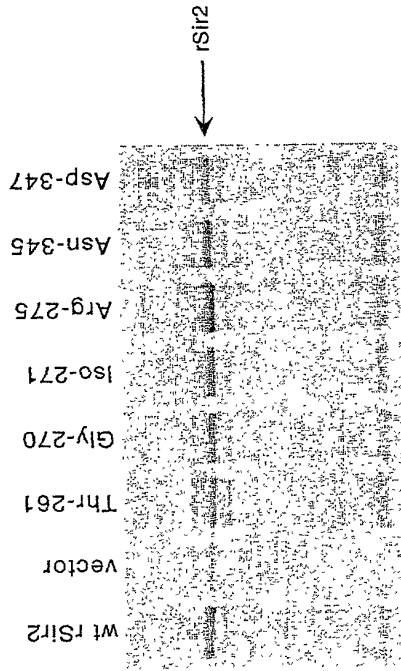


Figure 14b

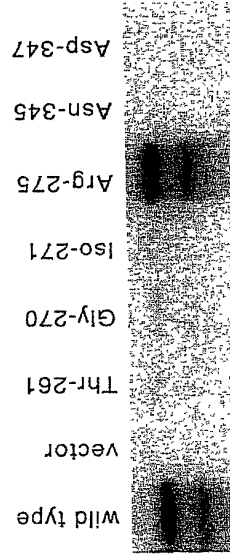


Figure 14c

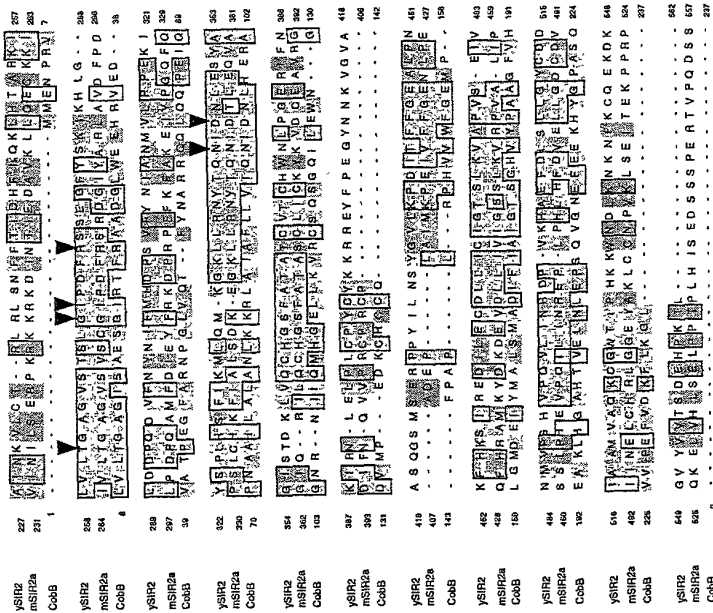


Figure 14a



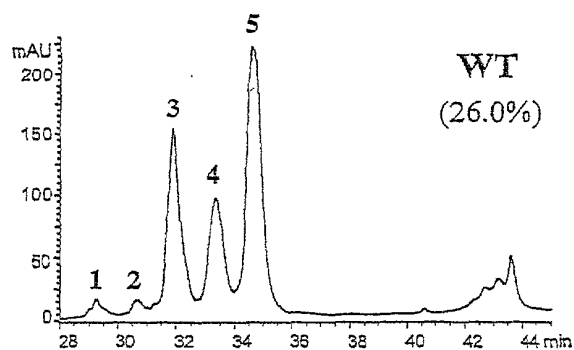


Figure 15a

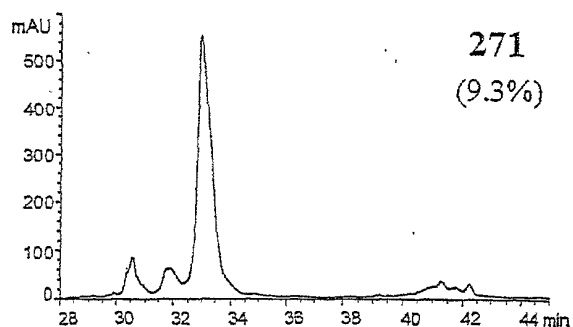


Figure 15e

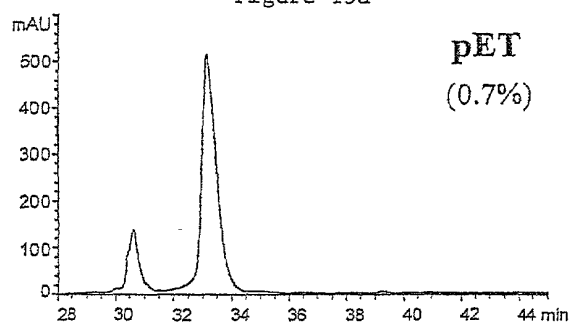


Figure 15b

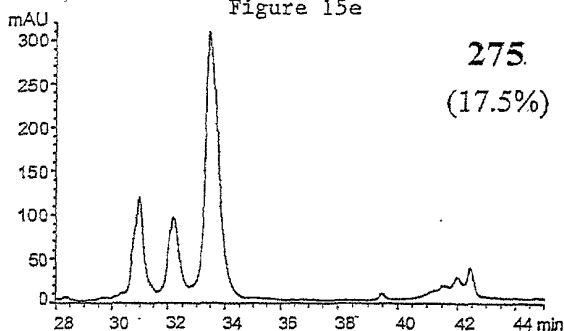


Figure 15f

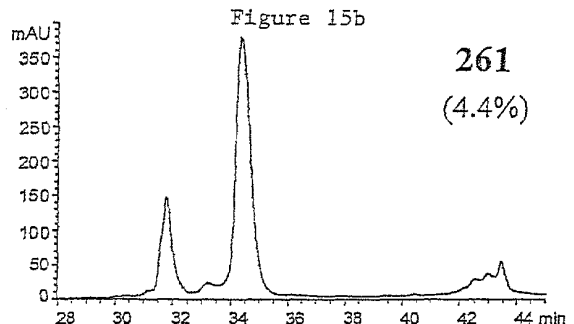


Figure 15c

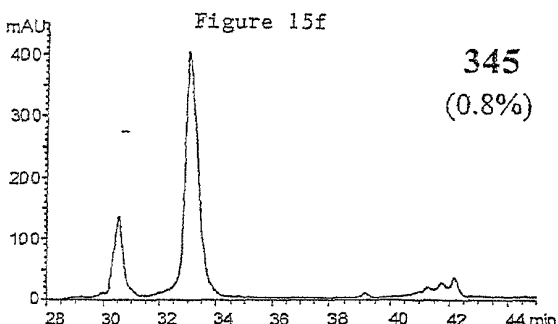


Figure 15g

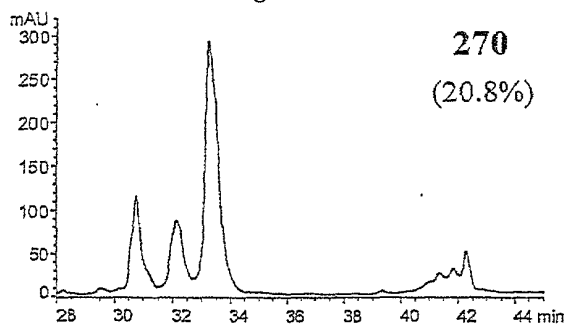


Figure 15d

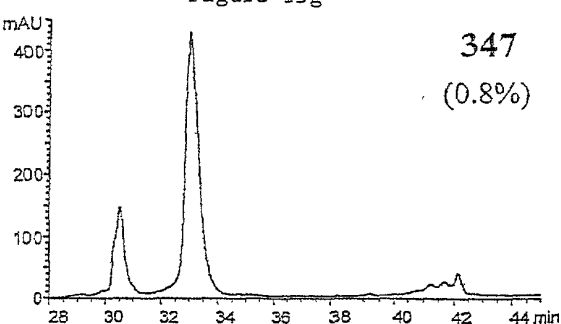


Figure 15h

201010-98/5E/60



Figure 16b

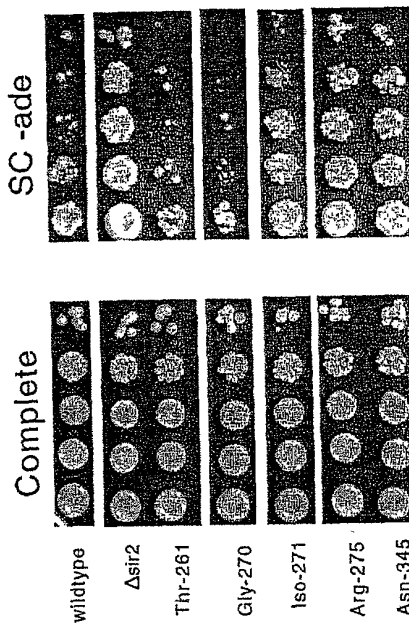


Figure 16d



Figure 16a

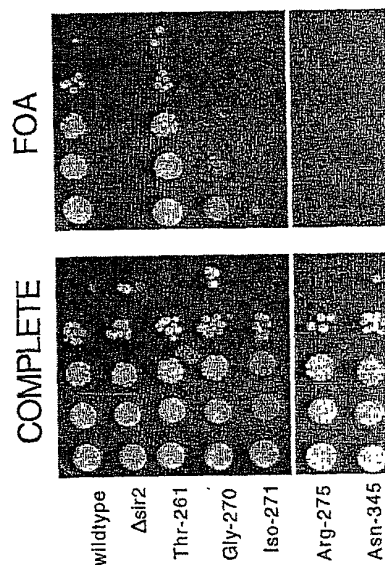


Figure 16c

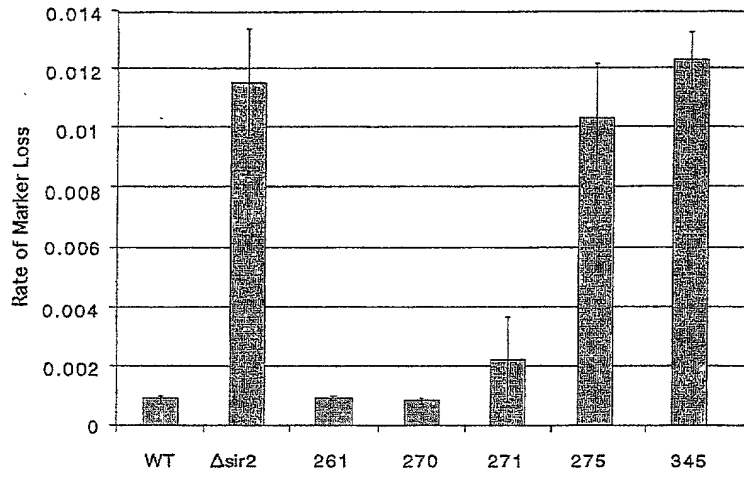


Figure 17a

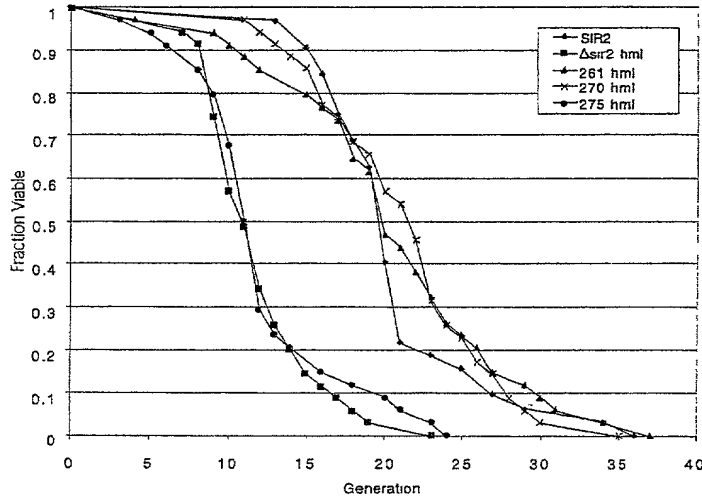


Figure 17b

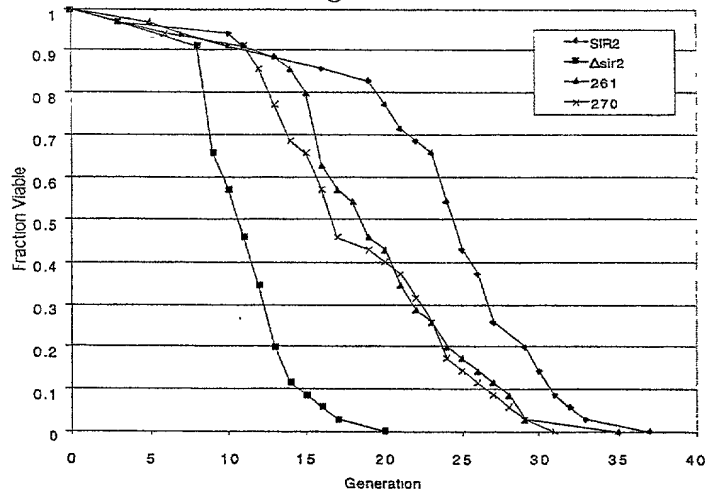


Figure 17c

201010" 98/55/60

| Mutant   | ADP-Rib.<br>Activity<br>(% of wt) | Deacetylase<br>Activity<br>(% of wt) | HM<br>Silencing | Telomere<br>Silencing | rDNA<br>Silencing | rDNA<br>Recombi-<br>nation | Mean<br>Life Span<br>(HML+) |
|----------|-----------------------------------|--------------------------------------|-----------------|-----------------------|-------------------|----------------------------|-----------------------------|
| sir2Δ    | 0%                                | 2.7%                                 | -               | -                     | -                 | 1.15%                      | 11.4                        |
| wildtype | 100%                              | 100%                                 | +               | +                     | +                 | 0.09%                      | 24.4                        |
| Thr-261  | 4%                                | 17%                                  | +               | +                     | +                 | 0.09%                      | 19.8                        |
| Gly-270  | 7%                                | 80%                                  | +               | +/-                   | +                 | 0.08%                      | 18.9                        |
| Iso-271  | 8%                                | 36%                                  | +               | -                     | +/-               | 0.22%                      | ND                          |
| Arg-275  | 100%                              | 67%                                  | -               | -                     | -                 | 1.03%                      | ND                          |
| Asn-345  | 0%                                | 3%                                   | -               | -                     | -                 | 1.22%                      | ND                          |
| Asp-347  | 0%                                | 3%                                   | -               | ND                    | ND                | ND                         | ND                          |

Figure 18

|            |     |                                                                         |     |
|------------|-----|-------------------------------------------------------------------------|-----|
| ySIR2      | 257 | I L V L T G A G V S T S L G I P D F R S - S E G F Y S K I K H - -       | 286 |
| yHST1      | 203 | I L V L T G A G V S T S L G I P D F R S - S E G F Y S K I R H - -       | 232 |
| yHST2      | 27  | V I F M V G A G I S T S C G I P D F R S P G T G L Y H N L A R - -       | 57  |
| yHST3      | 55  | I A C L T G A G I S C N A G I P D F R S - S D G L Y D L V K K D C       | 86  |
| yHST4      | 95  | M V V V S G A G I S V A A G I P D F R S - S E G I F S T V N G G S       | 126 |
| mSIR2alpha | 263 | I I V L T G A G V S V S C G I P D F R S - R D G L Y A R L A V D F       | 294 |
| mSIR2beta  | 79  | V I C L V G A G I S T S A G I P D F R S P S T G L Y A N L E K - -       | 109 |
| mSIR2g...  | 1   | - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -       | 10  |
| AI465098   | 48  | V V F H T G A G I S T A S C I P D F R G - P H G V W T M E E R - -       | 77  |
| AI465820   | 67  | L L V M T G A G I S T E S C I P D Y R S E K V G L Y A R T D R - -       | 97  |
| AI466061   | 59  | L A I S G A G V S A E S C V P T F R G - A G G Y W R K W Q A - -         | 88  |
|            |     |                                                                         |     |
| ySIR2      | 287 | - - - L G L D D P Q D V F N Y N I F M H D P S V - - F Y N I A N M       | 314 |
| yHST1      | 233 | - - - L G L E D P Q D V F N L D I F L Q D P S V - - F Y N I A H M       | 260 |
| yHST2      | 58  | - - - L K L P Y P E A V F D V D F E Q S D P L P - - F Y T L A K E       | 85  |
| yHST3      | 87  | S Q Y W S I K S G R E M E D I S L F R D D F K I S I E A K F E M E R     | 119 |
| yHST4      | 127 | - - - G K D L F D Y N R V Y G D E S M S L K F N - - Q L M V S L F       | 154 |
| mSIR2alpha | 295 | - - - P D L P D P Q A M F D I E Y F R K D P R P - - F F K F A K E       | 322 |
| mSIR2beta  | 110 | - - - Y H L P Y P E A I F E I S Y F K K H P E P - - F F A L A K E       | 137 |
| mSIR2g...  | 11  | - - - Y D I P Y P E A I F E L G F F F H N P K P - - F F M L A K E       | 38  |
| AI465098   | 78  | - - - G L A P K F D T I F E N A - - - - - - - - - - - - - - -           | 90  |
| AI465820   | 98  | - - - - - R P I Q - - H I D F V P V L R S A S G - - - - - - - -         | 114 |
| AI466061   | 89  | - - - Q D L A T P Q A F A R N P S Q V W E F Y H - - - - - Y R R E       | 113 |
|            |     |                                                                         |     |
| ySIR2      | 315 | V L P - - P E K I Y S P L H S F I K M L Q M K G K L L R N Y T Q N       | 345 |
| yHST1      | 261 | V L P - - P E N M Y S P L H S F I K M L Q D K G K L L R N Y T Q N       | 291 |
| yHST2      | 86  | L Y P - - G N F R P S K F H Y L L K L F Q D K D V L K R V Y T Q N       | 116 |
| yHST3      | 120 | L Y S N V Q L A K P T K T H K F I A H L K D R N K L L R C Y T Q N       | 152 |
| yHST4      | 155 | R L S - - K N C Q P T K F H E M L N E F A R D G R L L R L Y T Q N       | 185 |
| mSIR2alpha | 323 | I Y P - - G Q F Q P S L C H K F I A L S D K E G K L L R N Y T Q N       | 353 |
| mSIR2beta  | 138 | L Y P - - G Q F K P T I C H Y F I R L L K E K G L L L R C Y T Q N       | 168 |
| mSIR2g...  | 39  | L Y P - - G H Y R P N V T H Y F L R L L H D K E L L L R L Y T Q N       | 69  |
| AI465098   | 91  | - - - - - R - - P S K T H M A L V Q L E R M G F L S F L V S Q N         | 115 |
| AI465820   | 115 | T W P - - E N L W A G L N S P L T N P T Q H T W L - - - - - - -         | 137 |
| AI466061   | 114 | V M R - - S K - E P N P G H L A I A Q C E A R - - - - - - - - -         | 133 |
|            |     |                                                                         |     |
| ySIR2      | 346 | I D N L E S Y A G I S T D - - - - - - - - - - - - - - - K L V Q         | 362 |
| yHST1      | 292 | I D N L E S Y A G I D P D - - - - - - - - - - - - - - - K L V Q         | 308 |
| yHST2      | 117 | I D T L E R Q A G V K D D - - - - - - - - - - - - - - - L I E           | 133 |
| yHST3      | 153 | I D G L E E S I G L T L S N R K L P L T S F S S H W K N L D V V Q       | 185 |
| yHST4      | 186 | I D G L D T Q L P H L S T N - - - - - - - - - - V P L A K P I P S T V Q | 211 |
| mSIR2alpha | 354 | I D T L E Q V A G I Q R - - - - - - - - - - - - - - - I L Q             | 368 |
| mSIR2beta  | 169 | I D T L E R V A G L E P Q - - - - - - - - - - - - - - - D L V E         | 185 |
| mSIR2g...  | 70  | I D G L E R A S G I P A S - - - - - - - - - - - - - - - K L V E         | 86  |
| AI465098   | 116 | V D G L D V R S G F P R D - - - - - - - - - - - - - - - K L A E         | 132 |
| AI465820   | 0   | - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -             | 137 |
| AI466061   | 0   | - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -             | 133 |

Figure 19

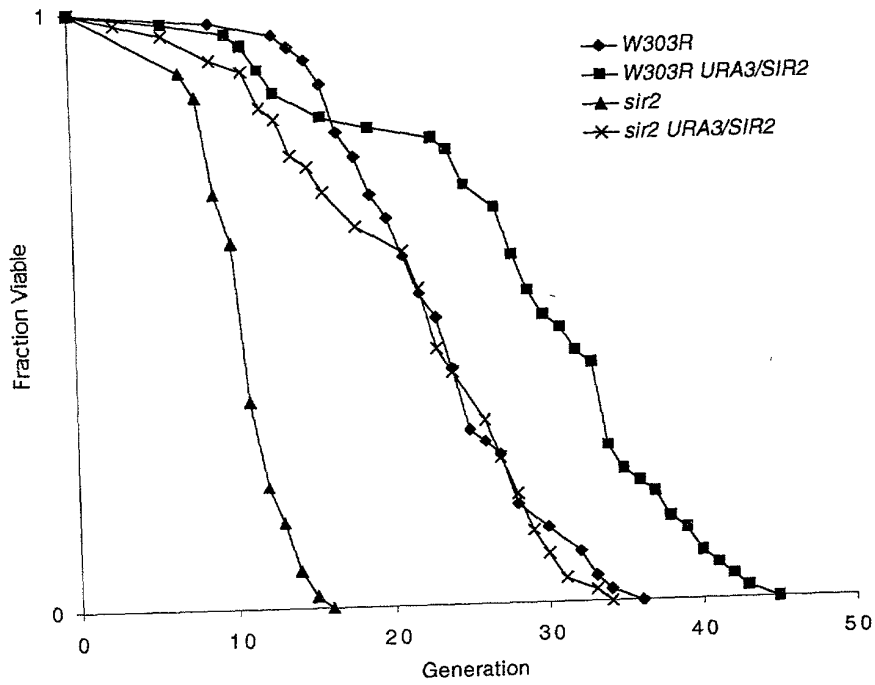


Figure 20

207040" 9875E260

10 20 30 40 50 60  
GCCGAGCAGAGGAGGCGGAGGGCGGAGGGCCAGAGAGGCAGTTGGAAGATGGCGGACGAGG  
M A D E V

70 80 90 100 110 120  
TGGCGCTCGCCCTTCAGGCCGCGGCTCCCTTCCGCGGCGGCGCCATGGAGGCCGCGT  
A L A L Q A A G S P S A A A A M E A A S

130 140 150 160 170 180  
CGCAGCCGCGGCGGACGAGCCGCTCCGCAAGAGGCCCGCGGAGACGGGCCTGGCCTCGGGC  
Q P A D E P L R K R P R R D G P G L G R

190 200 210 220 230 240  
GCAGCCCGGGCGAGCCGAGCGCAGCAGTGGCGCCGCGCGCGCGGGTGTGAGGCGGCGA  
S P G E P S A A V A P A A A G C E A A S

250 260 270 280 290 300  
GCGCCGCGGCCCCGCGGCGCTGTGGCGGGAGGCGGCAGGGCGCGCGGAGCGCGGAGC  
A A A P A A L W R E A A G A A A S A E R

310 320 330 340 350 360  
GGGAGGCCCCGCGGACGGCCGTGGCCGCGGACGGAGACAATGGGTCCGGCCTGCGGCGGG  
E A P A T A V A G D G D N G S G L R R E

370 380 390 400 410 420  
AGCCGAGGGCGGCTGACGACTTCGACGACGACGAGGGCGAGGAGGAGGACGAGGCGGCGG  
P R A A D D F D D D E G E E E D E A A A

430 440 450 460 470 480  
CGGCAGCGGCGGCGGCGGAGCGATCGGCTACCGAGACAACCTCCTGTTGACCGATGGACTCC  
A A A A A A I G Y R D N L L L T D G L L

490 500 510 520 530 540  
TCACTAATGGCTTTTCATTCTGTGAAAGTGATGACGATGACAGAACGTCACACGCCAGCT  
T N G F H S C E S D D D D R T S H A S S

550 560 570 580 590 600  
CTAGTGACTGGACTCCGCGGCGCGGATAGGTCCATATACTTTTGTTCAGCAACATCTCA  
S D W T P R P R I G P Y T F V Q Q H L M

610 620 630 640 650 660  
TGATTGGCACCGATCCTCGAACAATTCCTTAAAGATTTATTACCAGAAACAATTCCTCCAC  
I G T D P R T I L K D L L P E T I P P P

670 680 690 700 710 720  
CTGAGCTGGATGATATGACGCTGTGGCAGATTGTTATTAATATCCTTTTCAGAACCAACAA  
E L D D M T L W Q I V I N I L S E P P K

730 740 750 760 770 780  
AGCGGAAAAAAGAAAAAGATATCAATACAATTGAAGATGCTGTGAAGTTACTGCAGGAGT  
R K K R K D I N T I E D A V K L L Q E C

790 800 810 820 830 840  
GTAAAAAGATAATAGTTCTGACTGGAGCTGGGGTTTCTGTCTCCTGTGGGATTCTGACT  
K K I I V L T G A G V S V S C G I P D F

850 860 870 880 890 900  
TCAGATCAAGAGACGGTATCTATGCTCGCCTTGCGGTGGACTTCCCAGACCTCCCAGACC  
R S R D G I Y A R L A V D F P D L P D P

Figure 21a

09735786-040102

910 920 930 940 950 960  
CTCAAGCCATGTTTGATATTGAGTATTTTAGAAAAGACCCAAGACCATTCTTCAAGTTTG  
Q A M F D I E Y F R K D P R P F F K F A

970 980 990 1000 1010 1020  
CAAAGGAAATATATCCCGGACAGTTCCAGCCGTCTCTGTGTACAAATTCATAGCTTTGT  
K E I Y P G Q F Q P S L C H K F I A L S

1030 1040 1050 1060 1070 1080  
CAGATAAGGAAGGAAAACACTTCTCGAAATTATACTCAAAATATAGATACCTTGGAGCAGG  
D K E G K L L R N Y T Q N I D T L E Q V

1090 1100 1110 1120 1130 1140  
TTGCAGGAATCCAAAGGATCCTTCAGTGTTCATGGTTCTTTTGCAACAGCATCTTGCCTGA  
A G I Q R I L Q C H G S F A T A S C L I

1150 1160 1170 1180 1190 1200  
TTTGTAATAACAAAGTTGATTGTGAAGCTGTTCTGAGACATTTTAAATCAGGTAGTTC  
C K Y K V D C E A V R G D I F N Q V V P

1210 1220 1230 1240 1250 1260  
CTCGGTGCCCTAGGTGCCAGCTGATGAGCCACTTGCCATCATGAAGCCAGAGATTGTCT  
R C P R C P A D E P L A I M K P E I V F

1270 1280 1290 1300 1310 1320  
TCTTTGGTGAAAACCTTACCAGAACAGTTTCATAGAGCCATGAAGTATGACAAAGATGAAG  
F G E N L P E Q F H R A M K Y D K D E V

1330 1340 1350 1360 1370 1380  
TTGACCTCCTCATTTGTTATTTGGATCTTCTCTGAAAGTGAGACCAGTAGCACTAATTCCAA  
D L L I V I G S S L K V R P V A L I P S

1390 1400 1410 1420 1430 1440  
GTTCTATACCCCATGAAGTGCCTCAAATATTAAATAAATAGGGAACCTTTGCCTCATCTAC  
S I P H E V P Q I L I N R E P L P H L H

1450 1460 1470 1480 1490 1500  
ATTTTGATGTAGAGCTCCTTGGAGACTGCGATGTTATAATTAATGAGTTGTGTTCATAGGC  
F D V E L L G D C D V I I N E L C H R L

1510 1520 1530 1540 1550 1560  
TAGGTGGTGAAATATGCCAAACTTTGTTGTAACCCTGTAAAGCTTTCAGAAATTACTGAAA  
G G E Y A K L C C N P V K L S E I T E K

1570 1580 1590 1600 1610 1620  
AACCTCCACGCCCACAAAAGGAATTGGTTTCATTTATCAGAGTTGCCACCAACACCTCTTC  
P P R P Q K E L V H L S E L P P T P L H

1630 1640 1650 1660 1670 1680  
ATATTTTCGGAAGACTCAAGTTACCTGAAAGAACTGTACCACAAGACTCTTCTGTGATTG  
I S E D S S S P E R T V P Q D S S V I A

1690 1700 1710 1720 1730 1740  
CTACACTTGTAGACCAAGCAACAAACAATGTTAATGATTTAGAAGTATCTGAATCAA  
T L V D Q A T N N N V N D L E V S E S S

1750 1760 1770 1780 1790 1800  
GTTGTGTGGAAGAAAAACCACAAGAAGTACAGACTAGTAGGAATGTTGAGAACATTAAATG  
C V E E K P Q E V Q T S R N V E N I N V

1810 1820 1830 1840 1850 1860  
TGGAAAATCCAGATTTTAAGGCTGTTGGTTCCAGTACTGCAGACAAAAATGAAAGAACTT  
E N P D F K A V G S S T A D K N E R T S

1870 1880 1890 1900 1910 1920  
CAGTTGCAGAAACAGTGAGAAAATGCTGGCCTAATAGACTTGCAAAGGAGCAGATTAGTA  
V A E T V R K C W P N R L A K E Q I S K

Figure 21b

09735786-040102



App No.: 09/735,786  
Title: Methods for Identifying Agents ...  
Inventors: Leonard Guarente *et al.*

1930 1940 1950 1960 1970 1980  
AGCGGCTTGAGGGTAATCAATACCTGTTTGTACCACCAAATCGTTACATATTCACGGTG  
R L E G N Q Y L F V P P N R Y I F H G A

1990 2000 2010 2020 2030 2040  
CTGAGGTATACTCAGACTCTGAAGATGACGTCTTGTCTCTAGTTCTCTGTGGCAGTAACA  
E V Y S D S E D D V L S S S S C G S N S

2050 2060 2070 2080 2090 2100  
GTGACAGTGGCACATGCCAGAGTCCAAGTTTAGAAGAACCCTTGAAGATGAAAGTGAAA  
D S G T C Q S P S L E E P L E D E S E I

2110 2120 2130 2140 2150 2160  
TTGAAGAATTCTACAATGGCTTGAAGATGATACGAGAGGGCCGAATGTGCTGGAGGAT  
E E F Y N G L E D D T E R P E C A G G S

2170 2180 2190 2200 2210 2220  
CTGGATTTGGAGCTGATGGAGGGGATCAAGAGGTTGTTAATGAAGCTATAGCTACAAGAC  
G F G A D G G D Q E V V N E A I A T R Q

2230 2240 2250 2260 2270 2280  
AGGAATTGACAGATGTAACTATCCATCAGACAAATCATAACACTATTGAAGCTGTCCGG  
E L T D V N Y P S D K S \*

2290 2300 2310 2320 2330 2340  
ATTGAGGAATTGCTCCACCAGCATTTGGAACCTTTAGCATGTCAAAAAAATGAATGTTTAC

2350 2360 2370 2380 2390 2400  
TTGTGAACCTTGAACAAGGAAATCTGAAAGATGTATTTATTTATAGACTGGAAAATAGATTG

2410 2420 2430 2440 2450 2460  
TCTTCTTGGATAATTTCTAAAGTTCCATCATTTCTGTTTGTACTTGTACATTCACACTG

2470 2480 2490 2500 2510 2520  
TTGGTTGACTTCATCTTCCTTTCAAGGTTCAITTTGTATGATACATTTCGTATGTATGTATA

2530 2540 2550 2560 2570 2580  
ATTTTGTTTTTCCTAATGAGTTTCAACCTTTTAAAGTTTTCAAAAGCCATTGGAATGT

2590 2600 2610 2620 2630 2640  
TAATGTAAAGGGAACAGCTTATCTAGACCAAAGAATGGTATTTACACTTTTTTGTTTGT

2650 2660 2670 2680 2690 2700  
AACATTGAATAGTTTAAAGCCCTCAATTTCTGTTCTGCTGAACCTTTATTTTATAGGACAG

2710 2720 2730 2740 2750 2760  
TTAACTTTTAAACACTGGCATTTTCCAAAACCTTGTGGCAGCTAACTTTTAAATCACA

2770 2780 2790 2800 2810 2820  
GATGACTTGTAAATGTGAGGAGTCAGCACCGTGTCTGGAGCACTCAAACTTGGGCTCAGT

2830 2840 2850 2860 2870 2880  
GTGTGAAGCGTACTTACTGCATCGTTTTGTACTTGTCTGCAGACGTGGTAATGTCCAAAC

2890 2900 2910 2920 2930 2940  
AGGCCCTGAGACTAATCTGATAAATGATTTGGAAATGTGTTTCAGTTGTCTAGAAACA

2950 2960 2970 2980 2990 3000  
ATAGTGCTGTCTATATAGGTCCCCCTAGTTTGAATATTTGCCATTGTTTAAATTAAATAC

3010 3020 3030 3040 3050 3060  
CTATCACTGTGGTAGAGCCTGCATAGATCTTCACCACAAATACTGCCAAGATGTGAATAT

3070 3080 3090 3100 3110 3120  
GCAAAGCCTTTCTGAATCTAATAATGGTACTTCTACTGGGGAGAGTGTAATATTTTGGAC

3130 3140 3150 3160 3170 3180  
TGCTGTTTTTCCATTAATGAGGAAAGCAATAGGCCTCTTAATTAAAGTCCCAAAGTCATA

Figure 21c

09735786.040107

3190 3200 3210 3220 3230 3240  
AGATAAAATTGTAGCTCAACCAGAAAGTACACTGTTGCCCTGTTGAGGATTTGGTGTAATGT  
3250 3260 3270 3280 3290 3300  
ATCCCAAGGTGTTAGCCTTGTATTATGGAGATGAATACAGATCCAATAGTCAAATGAAAC  
3310 3320 3330 3340 3350 3360  
TAGTTCTTAGTTATTTAAAAGCTTAGCTTGCCCTTAAAAC TAGGGATCAATTTTCTCAACT  
3370 3380 3390 3400 3410 3420  
GCAGAAACTTTTAGCCTTTCAAACAGTTCACACCTCAGAAAGTCAGTATTTATTTTACAG  
3430 3440 3450 3460 3470 3480  
ACTTCTTTTGAACATTGCCCCCAAATTTAAATATTCATGTGGGTTTAGTATTTATTACAA  
3490 3500 3510 3520 3530 3540  
AAAAATGATTTGAAATATAGCTGTTCTTTATGCATAAAATACCCAGTTAGGACCATTACT  
3550 3560 3570 3580 3590 3600  
GCCAGAGGAGAAAAGTATTAAGTAGCTCAFTTCCCTACCTAAAAGATAACTGAATTTATT  
3610 3620 3630 3640 3650 3660  
TGGCTACACTAAAGAATGCAGTATATTTAGTTTTCATTTGCATGATGTGTTTGTGCTAT  
3670 3680 3690 3700 3710 3720  
AGACAATATTTTAAATTGAAAAATTTGTTTAAATATTTTACAGTGAAGACTGTTTTC  
3730 3740 3750 3760 3770 3780  
AGCTCTTTTATATTGTACATAGACTTTTATGTAATCTGGCATATGTTTTGTAGACCGTT  
3790 3800 3810 3820 3830 3840  
TAATGACTGGATTATCTTCCTCCAAC TTTGAAATACAAAAACAGTGTTTATACTAAAA  
3850 3860 3870  
AAAAAAAAAGTCGACGCGCGCGAATTC

Figure 21d

09735786.040102

10 20 30 40 50 60  
CCACGCGTCCGCGGACGCGTGGGCACGGGACAGAGCAGTCGGTGACAGTCCCCGAGGGCCC  
T R P R T R G H G T E Q S V T V P R A P

70 80 90 100 110 120  
CCACCCCGTTCCCATGGCCGAGCCGGACCGATTTCAGACTCGGACACTGAGGGAGGAGCCA  
T P F P W P S R T D S D S D T E G G A T

130 140 150 160 170 180  
CTGGTGGAGAGGCAGAGATGGACTTCCTGAGGAATTTATTCACCCAGACCCTGGGCCTGG  
G G E A E M D F L R N L F T Q T L G L G

190 200 210 220 230 240  
GTTCCCAAAGGAGCGTCTTCTAGACGAGCTGACCCTCGAAGGAGTGACACGCTACATGC  
S Q K E R L L D E L T L E G V T R Y M Q

250 260 270 280 290 300  
AGAGCGAGCGCTGCCGCAAGGTCATCTGTTTGGTGGGAGCCGGAATCTCCACGTCCGCGG  
S E R C R K V I C L V G A G I S T S A G

310 320 330 340 350 360  
GTATCCCTGACTTCCGCTCCCCGTCCACTGGCCTCTATGCAAACCTGGAGAAGTACCACC  
I P D F R S P S T G L Y A N L E K Y H L

370 380 390 400 410 420  
TTCCTTACCCAGAGGCCATCTTTGAGATCAGCTACTTCAAGAAACATCCGGAACCCCTTCT  
P Y P E A I F E I S Y F K K H P E P F F

430 440 450 460 470 480  
TTGCCCTTGCCAAGGAGCTCTATCCCGGGCAGTTCAAGCCAACCATCTGCCACTACTTCA  
A L A K E L Y P G Q F K P T I C H Y F I

490 500 510 520 530 540  
TCCGCCTGCTGAAGGAGAAGGGGCTGCTGCTGCGCTGCTACACGCAGAACATAGACACGC  
R L L K E K G L L L R C Y T Q N I D T L

550 560 570 580 590 600  
TGGAACGAGTGGCGGGGCTGGAGCCCCAGGACCTGGTGGAGGCCCCACGGCACCTTCTACA  
E R V A G L E P Q D L V E A H G T F Y T

610 620 630 640 650 660  
CATCACACTGTGTCAACACCTCCTGCAGAAAAGAATACACGATGGGCTGGATGAAAGAGA  
S H C V N T S C R K E Y T M G W M K E K

670 680 690 700  
AGATTTCTCAGAAGCAACTCCCAGGTGTGAGCAGTGTCA  
I S Q K Q L P G V S S V

Figure 22

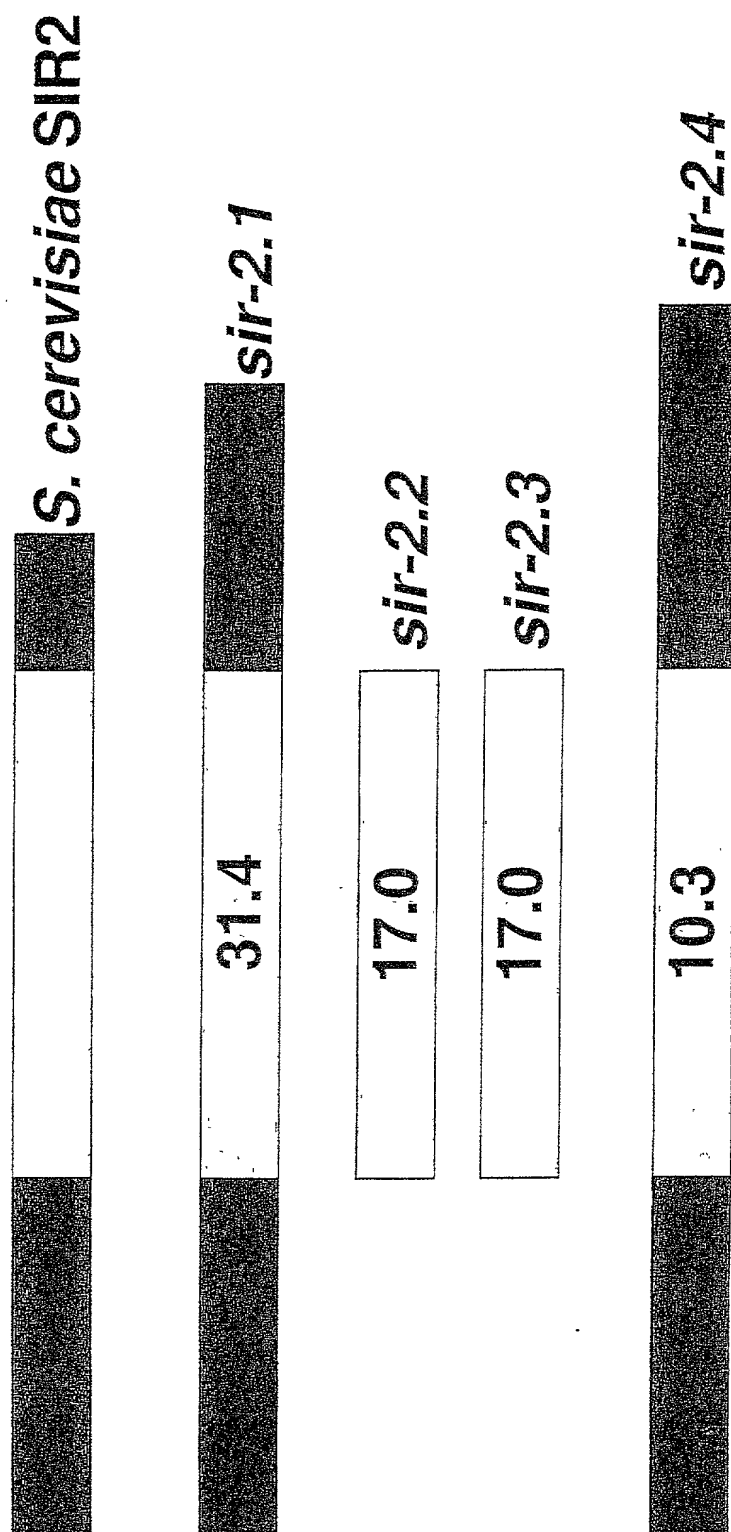


Figure 23

Figure 24A

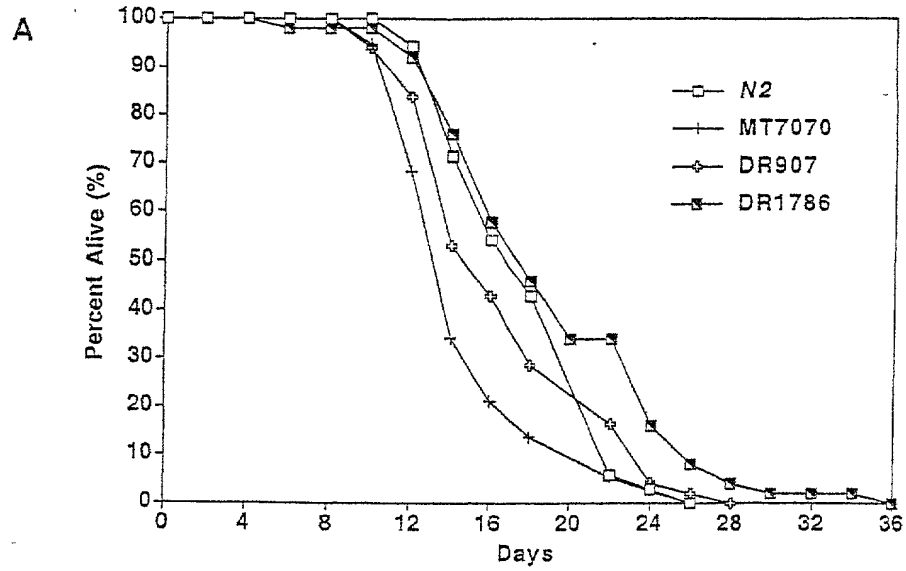


Figure 24B

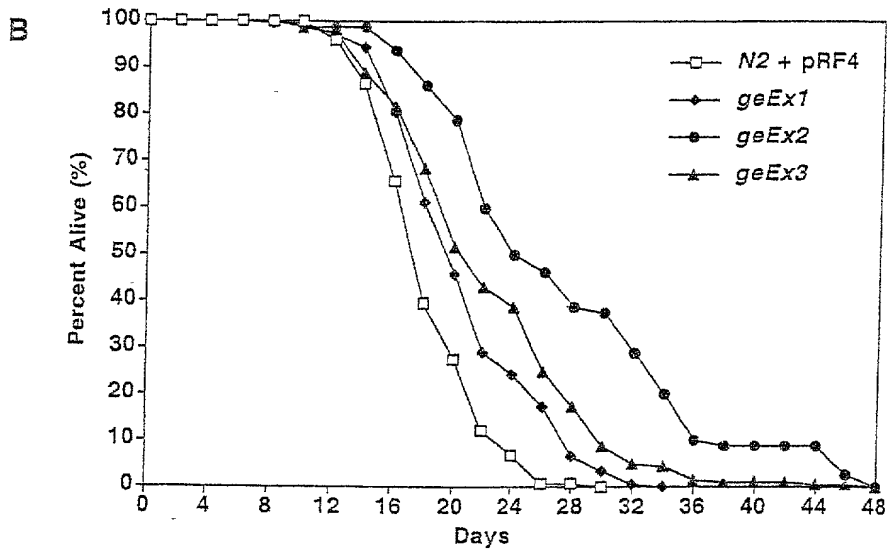


Figure 24C

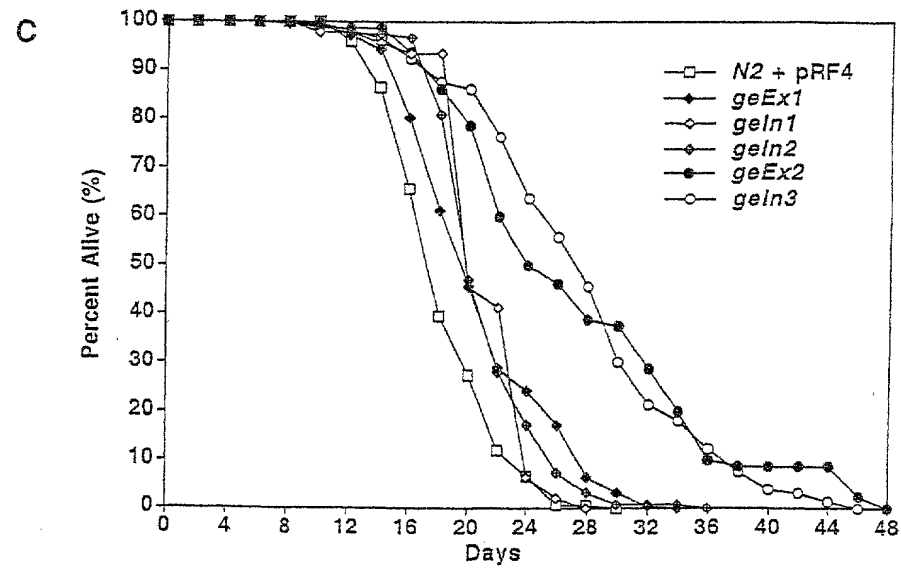


Figure 25A

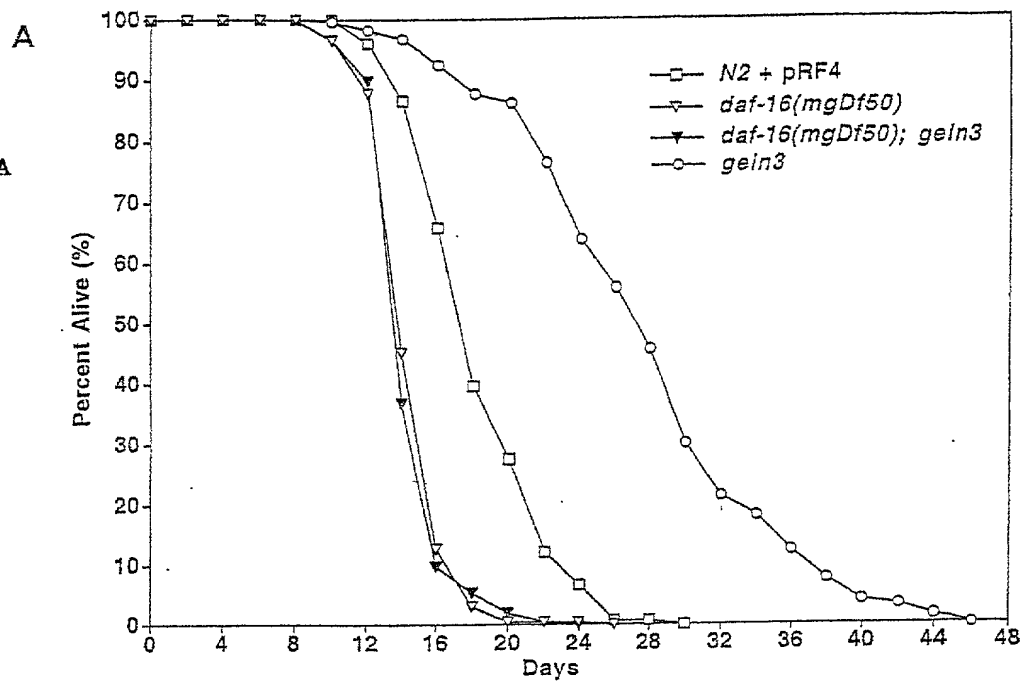


Figure 25B

